

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 17, 2004, 14:59:59 / Search time 103.667 Seconds

(without alignments)
804.784 Million cell updates/sec

Title: US-10-705-716a-2

Sequence: 1 MCGGSRADAEPRYBSWT.....VTENRQKDRKVTNRCIN 145

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1: uniprot_sp:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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32	83.5	10.9	700	2	030678	030678 xanthomonas
33	83.5	10.9	751	1	CNO3 MOUSB	Q8K0V4 mus musculus
34	83	10.8	561	2	0898T1	Q896L1 bradyrhizob
35	83	10.8	581	2	P89204	P89204 sugarcane m
36	83	10.8	1433	1	CAT8 YEAST	P39113 saccharomyc
37	82.5	10.8	514	2	Q78BP2	Q78BP2 neurospora
38	82.5	10.8	853	1	AOP2 MOUSB	Q6K688 mus muscu
39	82.5	10.8	879	2	BAC97980	BAC97980 mus muscu
40	82.5	10.7	1597	2	06KXP0	06KXP0 debaryomyce
41	82	10.7	339	2	06KXP5	06KXP5 streptomyce
42	82	10.7	882	1	AREA ASPMG	013412 aspergillus
43	82	10.7	882	2	CA68196	CA68196 aspergill
44	82	10.7	1449	2	Q7KPB1	Q7KPB1 oryza sativ
45	81.5	10.6	397	2	Q94KA7	Q94KA7 phaseolus v

ALIGNMENTS

RESULT 1						
ID	Q920K5	PRELIMINARY	PRT	145 AA		
AC	Q920K5					
DT	01-DRC-2001 (TREMELREL. 19, Created)					
DT	01-DRC-2001 (TREMELREL. 19, Last sequence update)					
DT	05-JUL-2004 (TREMELREL. 27, Last annotation update)					
DE	Dem-A20-4 (BAALC isoform 1-6-8)					
GN	Name-den-A20-4; Synonymus-BaalC;					
OS	Rattus norvegicus (Rat).					
OC	Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_Taxid=10116;					
PN	(1)					
RP	SEQUENCE FROM N.A.					
RA	Wang X., Tian Q., Li W., Okano A., Suzuki T.,					
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.					
RN	(2)					
RP	SEQUENCE FROM N.A.					
RC	STRALN-Bprague-Davley;					
RX	MEDLINE-21574584; PubMed-11707601;					
	Trimmer A W Biochem J T. 2000 357:1-10					

RA	Mrozek K., Gill H., Komutle S., Kolitz J.E., Archer K.J., Helmsen K.,
RB	"Genetic Basis of Human V.D.", <i>Journal of Virology</i> , 1987, 61(1), 1-11.
BA	Califant M.A., Bloomfield C.D., de la Chapelle A.,
RT	"BAC" the human member of a novel mammalian neuroectoderm gene
HL	lineage, is implicated in hematopoiesis and acute leukemia." <i>J.</i>
DR	Proc. Natl. Acad. Sci. U.S.A. 98(13501-13506(2001)).
DR	EMBL: AB073318; BAB0507.1; ..
DR	EMBL: AF371321; ALU50517.1; ..
DR	InterPro: IPR009728; BAAIC.N.
DR	Pfam: PF06989; BAAIC.N.1.
SO	SEQUENCE 145 AA; IS475 MW; DSA27AD67456F341 CRC64;

Query Match	100.0%	Score 7671	DB 2/	Length 145,
Best Local Similarity	100.0%	Prod. No. 3_4e-61,		
Matches 145,	Conservative 0,	Mismatches 0,	Indels 0,	Gaps 0

Df	1	MCCGGSRADAIERYRYEWSWETSTLTATTTSDALPSAAATTDSGPPAGGLHGVLEDP	60
Oy	1	MCCCGSRADAIERYRYEWSWETSTLTATTTSDALPSAAATTDSGPPAGGLHGVLEDP	60
Dd	61	SSNGVLPAPPGGIANPERKNNKCTOCENQSISLGGPILTYQNGNLMTTBARDARKMNR	120
Oy	61	SSNGVLPAPPGGIANPERKNNKCTOCENQSISLGGPILTYQNGNLMTTBARDARKMNR	120
Dd	61	SSNGVLPAPPGGIANPERKNNKCTOCENQSISLGGPILTYQNGNLMTTBARDARKMNR	120
Oy	121	EVAISTENTIRQMDRSKVTQNCLIN 145	
Dd	121	EVAISTENTIRQMDRSKVTQNCLIN 145	

RESULT 2		
ID	08AVYI	
CD	08AVYI	PRELIMINARY
AC	08AVYI	PRT: 145 AA.

RA	Mozek K., Gill R., Knutala S., Kolitz J.E., Archer K.J.,
RA	Caligiuri M.A., Bloomfield C.D., de la Chapelle A.,
RT	"BALC," the human member of a novel mammalian neuroectoderm gene
RT	lineage, is implicated in hematopoiesis and acute leukemia."
HL	Proc. Natl Acad Sci. U.S.A. 98:13901-13906(2001).
DR	HMBL; AB073319; BAB70507.1;"
DR	HMBL; AF371321; MAL50517.1;"
DR	Interpretor: IPK009728; BALC_N.
DR	Pfam: PF00989; BALC_N_1.
SO	SEQUENCE .145 AA; I5475 MW; D5A27AD67456F341 CRC64;
Query Match	100.0%; Score 767; DB 2; Length 145;
Best Local Similarity	100.0%; Pred. No. 3,4e-61;
Matches 145; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Cy	1 HCGGSRBDALPEPTYSWTRSTETSLTTTDSNALPSAAATSGSAGATACGTACGP 60
Dd	1 MCCGGSRBDALPEPTYSWTRSTETSLTTTDSNALPSAAATSGSAGATACGTACGP 60
Cy	61 SENGTLAPAAPQGIANPERKKMGCTCCNSOSLSGGPLVIXONGLTATTAKDARDMSAR 120
Dd	61 SENGTLAPAAPQGIANPERKKMGCTCCNSOSLSGGPLVIXONGLTATTAKDARDMSAR 120
Cy	121 SVALSVENTIKMDRSKRVTYCNIN 145
Dd	121 EVALTENTINKMDRSKRVTNCIN 145
RESULT 2	
08AVH1	PRELIMINARY; PRT; 145 AA.
ID	
AC	08AVH1,

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01-MAR-2002 (TIGRBLrefl. 20, Created)
01-MAR-2002 (TIGRBLrefl. 20, Last sequence update)
01-OCT-2004 (TIGRBLrefl. 28, Last annotation update)
BLINK Inform 1-E-8. (Mus musculus 16 days neonate cerebellum cDNA,
Riken full-length enriched library, cDNA:963002H16 product:brain and
de acute leukemia, cytoplasmic, full insert sequence).
GN Name=Balc1;
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TIGSUB=Cerebellum;
RX MEDLINE=11574584; PubMed=11707601;
RA Tanner S.W., Austin J.T., Leone G., Rush L.J., Plase C., Helminen K.,
RA Moore K.M., Gill H., Knutti S., Kolfer J.B., Archer K.J.,
RA Califugi M.A., Bloomfield C.D., de la Chapelle A.,
RA Shale, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:113901-113906(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TIGSUB=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carminci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Nucleic. Acids. Res. 27:139-144(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TIGSUB=Cerebellum;
RX MEDLINE=11085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TIGSUB=Cerebellum;
RA The PANTOM Consortium,
RT "The Riken Genome Exploration Research Group Phase I & II Team,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TIGSUB=Cerebellum;
RX MEDLINE=1049374; PubMed=11042159;
RA Carminci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RL "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TIGSUB=Cerebellum;
RX MEDLINE=10530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carminci P.,
RA Kono H., Akiyama J., Nishi K., Kitunai T., Tashiro H., Itoh M.,
RA Saito M., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujitake S., Ito H., Togawa Y., Iwata M., Ohara E., Matsubara S., Kawai J.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuyama S., Kawai J.,
RA Okazaki Y., Muramatsu M., Ito H., Kita A., Hayashizaki Y.,
RT "Riken integrated sequence analysis (RISA) system:384-format
RT sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TIGSUB=Cerebellum;
RX MEDLINE=10530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carminci P.,
RA Kono H., Akiyama J., Nishi K., Kitunai T., Tashiro H., Itoh M.,
RA Saito M., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujitake S., Ito H., Togawa Y., Iwata M., Ohara E., Matsubara S., Kawai J.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuyama S., Kawai J.,
RA Okazaki Y., Muramatsu M., Ito H., Kita A., Hayashizaki Y.,
RT "Riken integrated sequence analysis (RISA) system:384-format
RT sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771(2000).

RA	Katoh H., Kawai Y., Kojima Y., Kondo S., Komoto H., Konda M., Koye S.,
RA	Rathore A., Maruyama T., Miyazaki A., Murata M., Nakamura M.,
RA	Nishi K., Nomura K., Numasaki R., Ohno M., Ohsato N., Okazaki Y.,
RA	Saito K., Satoh H., Sakai C., Sakai F., Sakuma N., Sano H.,
RA	Seikai D., Shibata K., Shingawa A., Shiraki A., Tagami Y., Tagami M.,
RA	Togawa A., Takahashi Y., Takasu-Akita M., Tanabe T., Tanaka T.,
RA	Tomaru A., Toya T., Yasunishi A., Yamamoto M., Hayashizaki Y.,
RL	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AP371320; AAC50516.1;
DR	EMBL; AK079337; BAC37611.1;
DR	MED; MG11928704; BaalC.
DR	InterPro; IPRO09728; BAALC.N.
DR	Pfam; PF06989; BAALC.N; 1.
DR	SEQUENCE 145 AA; 15515 MW; 4976270A618CDAD6 CRC64;
Query Match	92.3% Score 7461 DB 21 Length 1451
Best Local Similarity	97.6% Prod. NO. 2.7e-59;
Matches 141;	Conservative 21 Miscellaneous 31 Indels 0 Gaps 0
CY	1 MGCGSRDADPRATRYBSWTRRTSTLTLYTDSGLPSAAATGSGPBAAGCLHAGTLEOP 60
DB	1 MGCGSRDADPRATRYBSWTRRTSTLTLYTDSGLPSAAATGSGPBAAGCLHAGTLEO 60
CY	61 SSNGVLPAPAPGQIANPEKKNCCCTCCPNSSQSLSSGPLTOXKNGILTTTPAKXDARMSAR 120
DB	61 SSNGVLPAPAPGQIANPEKKNCCCTCCPNSSQSLSSGPLTOXKNGILTTTPAKXDARMSAR 120
CY	121 EVAVSTETIRICMDSRRVTNCSIN 145
DB	121 EVAVSTETIRICMDSRRVTNCSIN 145
RESULT 3	
ID	G9HA93 PRELIMINARY PRF, 145 AA.
AC	G9HA93;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Hypothetical protein FLJ12015 (BAAIC Isoform 1-6-8) (Brain and acute
DE	leukemia; Cytoplasmic) (BAAIC 1-6-8).
GN	Name=BAAIC;
OS	Human sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_Taxid=9606;
RP	[1]
RN	SOURCE FROM N.A.
RC	Tissue-whole embryo/
RX	PubMed:14702039;
RA	Ota T., Suzuki Y., Nishikawa T., Otsubu T., Sugiyama T., Irie R.,
RA	Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Mathe H.,
RA	Seike N., Okeyoshi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA	Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Noguchi A.,
RA	Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA	Budo H., Hosoi T., Kakui Y., Kodaira H., Kondo H., Sugawara M.,
RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA	Abe K., Kamihara K., Katenuka N., Sato K., Tanikawa M., Yamazaki M.,
RA	Ninomiya K., Ichibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA	Tanai H., Kimura M., Matsubae M., Hiratsuka S., Chiba Y., Ishida S.,
RA	Ono Y., Takiguchi S., Matsubae S., Yoshida M., Horuta T., Kusano J.,
RA	Kanehori K., Takahashi-Puji A., Hara H., Tanase T., Nomura Y.,
RA	Tojiya S., Komai F., Hara K., Takeuchi K., Arima M., Imose N.,
RA	Yoshitake Y., Matsunawa H., Ichihara T., Shiota N., Seno S.,
RA	Motoki S., Momiyama H., Satoh N., Takami T., Terashima Y., Suzuki O.,
RA	Hinagaki S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA	Hinagaki M., Matsubae T., Sugiyama A., Takemoto M., Kawakami B.,
RA	Yamazaki M., Matsuyama K., Kumagai A., Itakura S., Fukusumi Y.,
RA	Fujimori Y., Komiyama M., Tasuhira H., Tanigami A., Fujisawa T.,
RA	Ono T., Yamada K., Fujii Y., Osaki K., Hiro M., Ohmori Y.,
RA	Kawabata A., Hikiji T., Kobayashi N., Inagaki H., Ikema Y., Okamoto S.,
RA	Okutani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Genda T.,